IN THE CLAIMS:

Please cancel claims 40 and 41, without prejudice or disclaimer.

Please amend claim 30 as follows:

-- 30 [Amended]. A method for analyzing DNA for the presence of a polymorphic site, said site being [identifying] a single nucleotide polymorphic site, wherein said method [which] comprises:

A) isolating a fragment of genomic DNA of a reference organism;

B) sequencing said fragment of DNA to thereby determine the nucleotide sequence of a segment of said fragment, said segment being of a length sufficient to define the nucleotide sequence of a pair of oligonucleotide primers capable of mediating the specific amplification of said fragment;

C) using said oligonucleotide primers to mediate the specific amplification of DNA obtained from a plurality of other organisms of the same species as said reference organism; and

D) determining the nucleotide sequences of said amplified DNA molecules of step C, and comparing the sequence of said amplified molecules with the sequence of said fragment of said reference organism to thereby identify a single nucleotide polymorphic site. --

Please amend claim 31 as follows:

-- 31 [Three Times Amended]. A method for analyzing DNA of a target human by identifying [the single nucleotide present at] a polymorphic region of [a human single nucleotide polymorphism of a] said target human, said method comprising the steps:

(A) selecting a human single nucleotide polymorphism for such analysis [identification];

(B) identifying the sequence of at least one oligonucleotide that flanks said selected single nucleotide polymorphism; said identified sequence being of a length sufficient to permit the identification of primers capable of being used to effect the specific amplification of said flanking oligonucleotide and said polymorphism;

(C) using said primers to effect the amplification of said flanking oligonucleotide and said polymorphism of said single nucleotide polymorphism of said target human; and

(D) identifying the single nucleotide present at the single nucleotide polymorphism of said amplified polymorphism by genetic bit analysis, wherein said genetic bit analysis comprises the substeps:

(a) incubating a sample of nucleic acid containing said single nucleotide polymorphism of said target human in the presence of a nucleic acid primer and from one to four dideoxynucleotide derivatives, under conditions sufficient to permit a polymerase mediated, template-dependent extension of said primer, said extension causing the incorporation of a single dideoxynucleotide derivative to the 3′-terminus of said primer, said incorporated single dideoxynucleotide derivative being complementary to the single nucleotide of the polymorphic site of said polymorphism;

(b) permitting said template-dependent extension of said primer molecule, and said incorporation of said single dideoxynucleotide derivative; and

(c) determining the identity of said single nucleotide of said nucleotide polymorphism by determining the identity of the dideoxynucleotide derivative incorporated into said primer, said identified dideoxynucleotide derivative being complementary to said single nucleotide of said polymorphism. --

Please amend claims 42 as follows:

-- 42 [Amended]. The method of claim 37, wherein said determination of step (F) comprises the substeps:

(i) determining the identity of a single nucleotide present at a polymorphic site of a[n equine] <u>human</u> single nucleotide polymorphism, and being present in more than 51% of a set of reference humans;

(ii) determining whether a single nucleotide present at a polymorphic site of a corresponding single nucleotide polymorphism of said target human has the same identity as the single nucleotide present at said polymorphic site of said 51% of reference humans exhibiting said trait; and

(iii) [using said determination of substep (ii) to determine] <u>determining</u> whether said target human will have said [particular] trait. --

Please amend claim 45 as follows:

-- 45 [Amended]. A method for creating a genetic map of unique sequence [equine] human polymorphisms which comprises the steps:

(A) identifying at least one pair of inter-breeding reference humans, wherein each of said pairs of humans is characterized by having a first and a second reference human,

said first reference human having:

two alleles (i) and (ii), said alleles each being single nucleotide polymorphic alleles having a single nucleotide polymorphic site;

said second reference human having:

a corresponding allele (i') to said allele (i) of said first reference human, wherein said allele (i') has a single nucleotide polymorphic site, and wherein the single nucleotide present at said polymorphic site of said allele (i') differs from the single nucleotide present at the polymorphic site of said allele (i) of said first reference human, and

(B) identifying in a progeny of at least one of said pairs of inter-breeding reference humans the single nucleotide present at a single nucleotide polymorphic site of a corresponding allele of said alleles (i) and (i'), and the single nucleotide present at a single nucleotide polymorphic site of a corresponding allele of said alleles (ii) and (ii'); and

(C) determining the extent of genetic linkage between said alleles (i) and (ii), to thereby create said a genetic map. --

REMARKS

I. Status Of The Application

Claims 30-38 and 40-46 were pending, claims 40 and 41 have been canceled without prejudice or disclaimer and no new claims have been added. Thus, claims 30-38 and 43-46 are pending.